

10 30 50
 TCACTCATTGTGAAAGCTGAGCTCACAGCCGAATAAGCCACCATGAGGCTGTCAGTGTGT
 M R L S V C
 70 90 110
 CTCCTGATGGTCTCGCTGGCCCTTTGCTGCTACCAGGCCCATGCTCTTGTCTGCCAGCT
 L L M V S L A L C C Y Q A H A L V C P A
 130 150 170
 GTTGCTTCTGAGATCACAGTCTTCTTATTCTTAAGTGACGCTGCGGTAAACCTCCAAGTT
 V A S E I T V F L F L S D A A V N L Q V
 190 210 230
 GCCAACTTAATCCACCTCCAGAAGCTCTTGCAGCCAAGTTGGAAGTGAAGCACTGCACC
 A K L N P P P E A L A A K L E V K H C T
 250 270 290
 GATCAGATATCTTTAAGAAACGACTCTCATTGAAAAAGTCCTGGTGAAATAGTGA
 D Q I S F K K R L S L E K V L V E I V K
 310 330 350
 AAATGTGGTGTGTGACATGTAAAAATGCTCAACCTGGTTCCAAAGTCTTTCAACGACAC
 K C G V
 370 390 410
 CCTGATCTTCACTAAAAATTGTAAAGGTTTCAACAGTTGCTTTAATAAATCACTTGCCC
 430
 TGCACATCAAAAA

FIG.1

10 30 50
 TTGTTTGTGAAAGCTGAGCTCACAGCAAAACAAGCCACCATGAAGCTGTGGTGTGTCTC
 M K L S V C L
 70 90 110
 CTGCTGGTCACGCTGGCCCTCTGCTGCTACCAGGCCAATGCCGAGTTCTGCCAGCTCTT
 L L V T L A L C C Y Q A N A E F C P A L
 130 150 170
 GTTCTGAGCTGTTAGACTTCTTCTTCATTAGTGAACCTCTGTTCAAGTTAAGTCTTGCC
 V S E L L D F F F I S E P L F K L S L A
 190 210 230
 AAATTTGATGCCCCTCCGAAGCTGTTGCAGCCAAGTTAGGAGTGAAGAGATGCACGGAT
 K F D A P P E A V A A K L G V K R C T D
 250 270 290
 CAGATGTCCCTTCAGAAACGAAGCCTCATTGCCGAAGTCCTGGTGAAAATATTGAAGAAA
 Q M S L Q K R S L I A E V L V K I L K K
 310 330 350
 TGTAGTGTGTGACATGTAAAACTTTCATCCTGGTTTCCACTGTCTTTCAATGACACCCT
 C S V
 370 390 410
 GATCTTCACTGCAGAATGTAAAGGTTTCAACGTCTTGCTTTAATAAATCACTTGCTCTCC
 430
 AAAAAAAAAAAAAA

FIG.2

10 30 50
 ACGAGCTGCCACGCACGACTGAACACAGACAGCAGCCGCCTCGCCATGAAGCTGCTGATG
 M K L L M
 70 90 110
 GTCCTCATGCTGGCGGCCCTCCTCCTGCACTGCTATGCAGATTCTGGCTGCAAACCTCTG
 V L M L A A L L L H C Y A D S G C K L L
 130 150 170
 GAGGACATGGTTGAAAAGACCATCAATTCCGACATATCTATACCTGAATACAAAGAGCTT
 E D M V E K T I N S D I S I P E Y K E L
 190 210 230
 CTTCAAGAGTTCATAGACAGTGATGCCGCTGCAGAGGCTATGGGGAAATTCAAGCAGTGT
 L Q E F I D S D A A A E A M G K F K Q C
 250 270 290
 TTCCTCAACCAGTCACATAGAACTCTGAAAACTTTGGACTGATGATGCATACAGTGTAC
 F L N Q S H R T L K N F G L M M H T V Y
 310 330 350
 GACAGCATTTGGTGTAAATATGAAGAGTAATTAACCTTTACCCAAGGCGTTTGGCTCAGAGG
 D S I W C N M K S N *
 370 390 410
 GCTACAGACTATGGCCAGAACTCATCTGTTGATTGCTAGAAACCACTTCTTCTTGTGTT
 430 450 470
 GCTTTTATGTGGAACTGCTAGACAAGTGTGAAACCTCAATTCATTCCATTTC

FIG.3

1 MRLSVCLLMVSLALCCYQAHA.LVCPAVASEITVFLFLSDAAVNQLQAKL 49
 : ||:||||: ||:||||:| | :|. || |.. ||: |...: :....
 4 ielslcilim.lavccyeanasqicelvahtisflmkseeelkkelemy 52
 50 NPPPEALAAKLEVKHCTDQISFKKRLSLEKVLVEIVKKCGV 90
 |:|:|:|||||:|:|:| | .|| :...|| |. .|||
 53 nappaaveaklevkrcevdqmsngdrlvvaetlvviflecgv 93

FIG.4

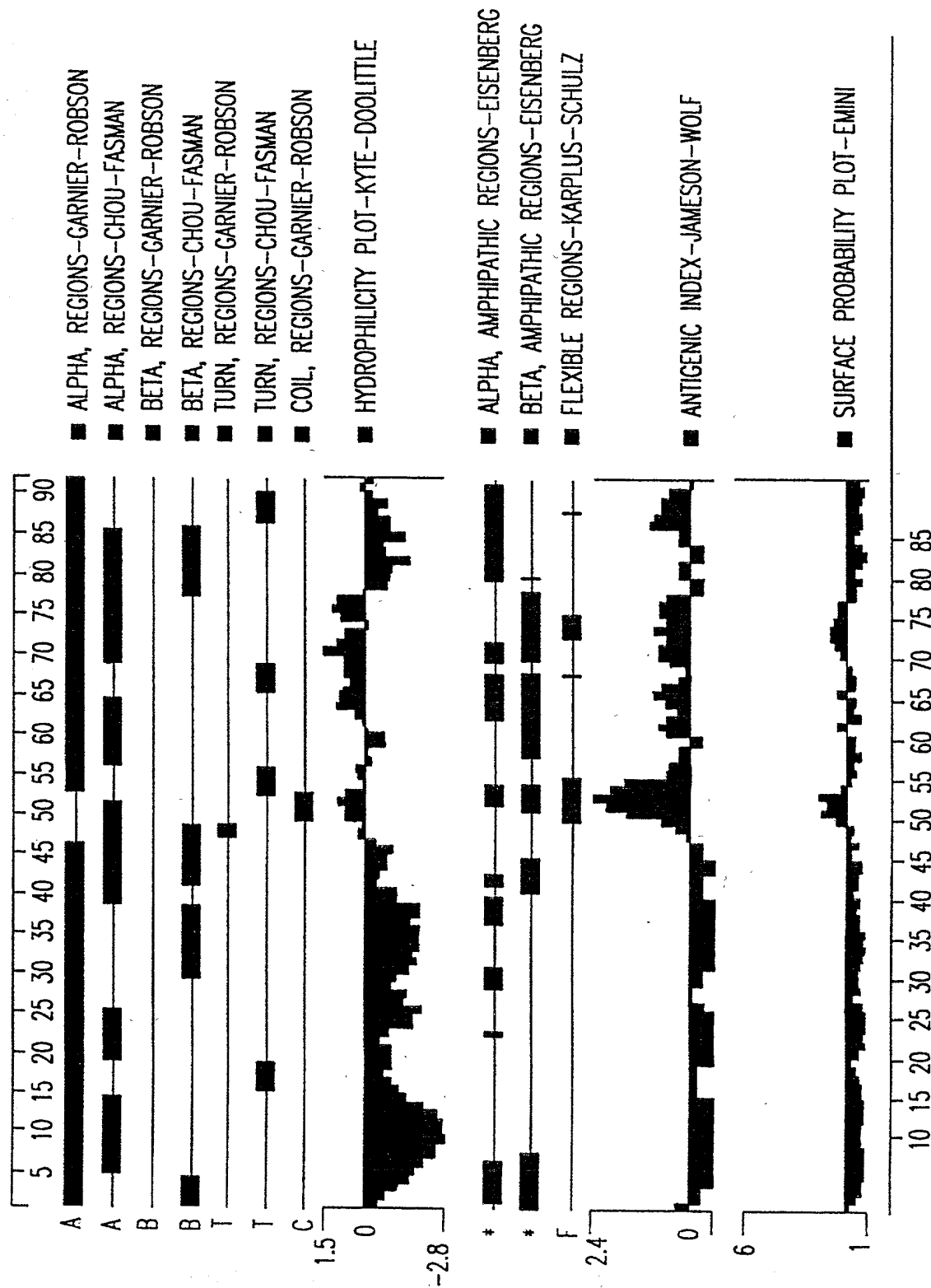


FIG.7

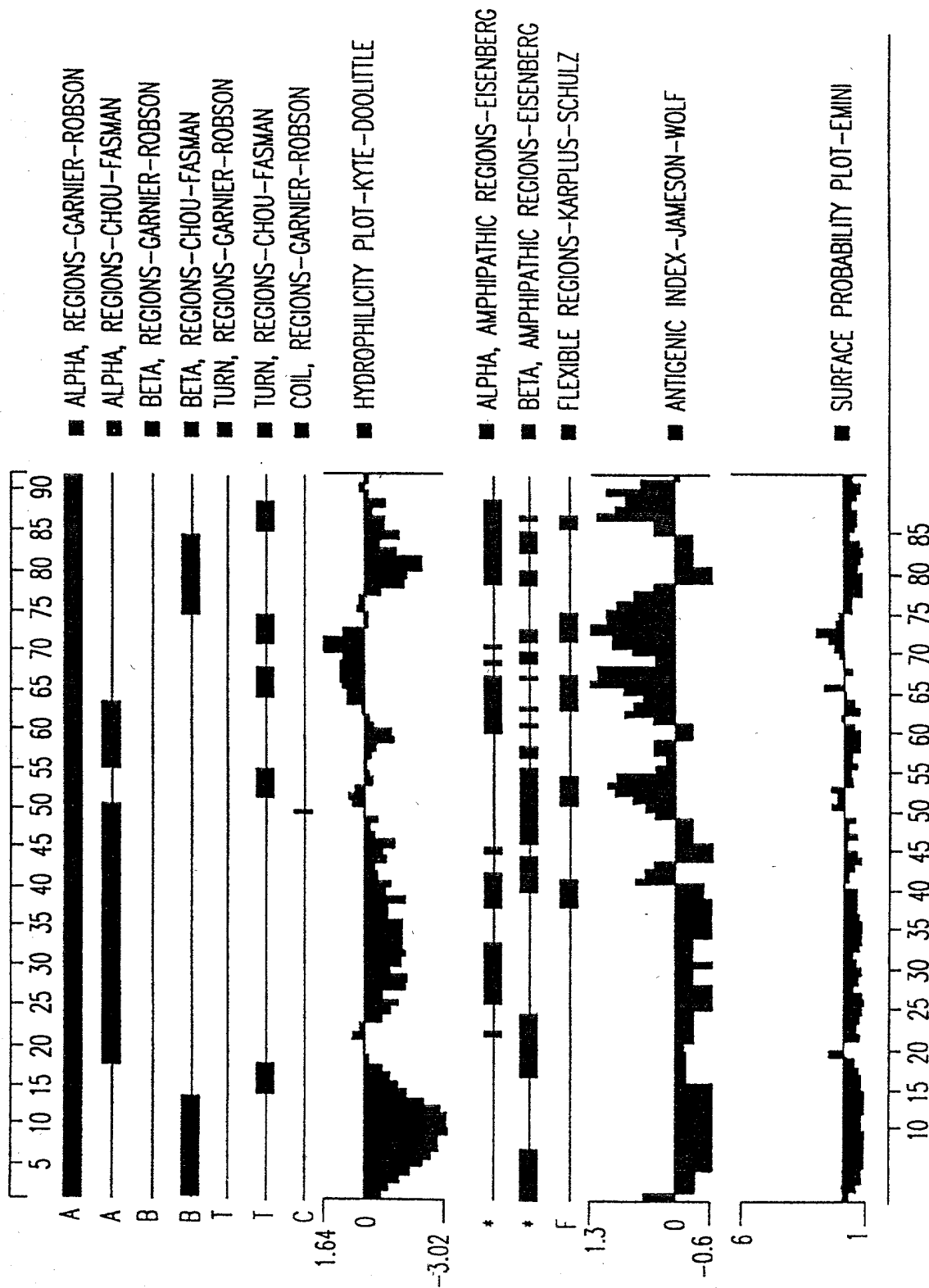


FIG.8

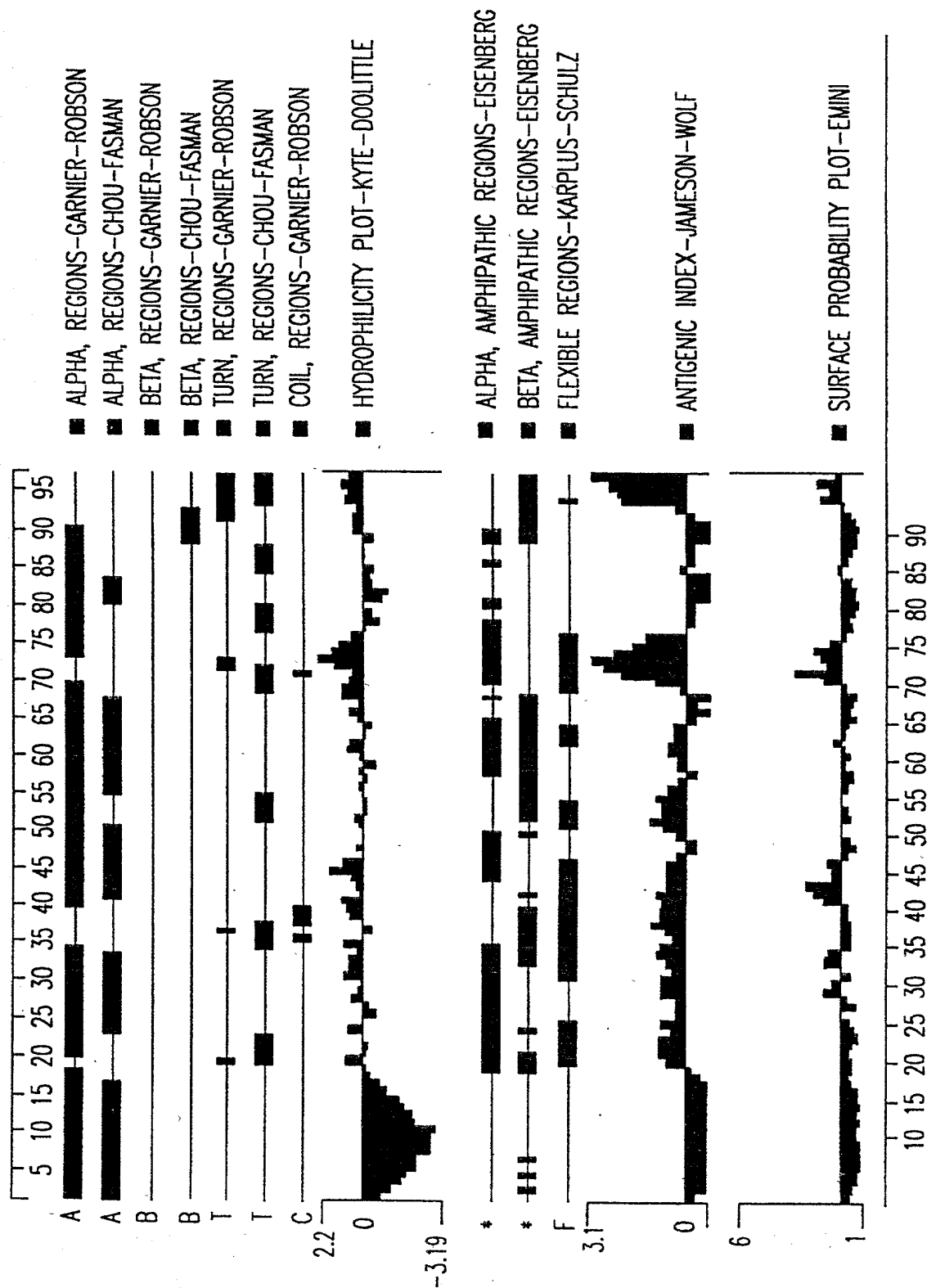


FIG.9